

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:24:09 ; Search time 120.319 Seconds
(without alignments)
5689.057 Million cell updates/sec

Title: US-09-625-573-1
Perfect score: 2232
Sequence: 1 GGATGTGAACAGGACGATT.....TATAACTATGTTGATAAAAG 2232

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2.6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2232	100.0	2232	1	US-08-450-393A-1
2	2232	100.0	2232	3	US-08-446-669-1
3	2232	100.0	2232	5	PCT-US95-00476-1
4	980	43.9	1979	1	US-08-450-393A-3
5	980	43.9	1979	3	US-08-446-669-3
6	980	43.9	1979	5	PCT-US95-00476-3
7	635.6	28.3	1059	4	US-09-517-605-8
8	632.6	28.3	1059	4	US-08-724-984A-3
9	632.6	28.3	1071	3	US-09-087-232A-14
10	632.6	28.3	1376	3	US-09-087-232A-12
11	632.6	28.3	1477	4	US-08-833-752-2
12	632.6	28.3	3383	4	US-08-861-105-13
13	632.6	28.3	3383	4	US-08-575-967A-1
14	632.6	28.3	5674	4	US-09-293-170-3
15	629.4	28.2	1414	3	US-08-466-343D-1
16	612.6	27.4	1344	3	US-09-087-232A-16
17	612.6	27.4	1442	4	US-08-833-752-3
18	588.2	26.4	2440	4	US-08-724-984A-1
19	376	16.8	792	1	US-08-833-752-1
20	325	14.6	2156	1	US-08-012-988A-1
21	323.4	14.5	1085	4	US-08-847-296B-2
22	323.4	14.5	1915	4	US-08-575-967A-3
23	308.6	13.8	461	3	US-09-087-232A-11
24	288.4	12.9	1607	3	US-08-875-573-19
25	288.4	12.9	1695	4	US-09-232-878-1
26	264	11.8	1161	1	US-08-153-848-31
27	264	11.8	1161	5	PCT-US93-11153-31

28 264 11.8 2254 1 US-08-153-848-27 Sequence 27, Appl
29 264 11.8 2254 3 US-09-299-843A-27 Sequence 27, Appl
30 264 11.8 2254 4 US-09-088-337B-27 Sequence 27, Appl
31 264 11.8 2254 5 PCT-US93-11153-27 Sequence 31, Appl
32 264 11.8 3119 3 US-09-299-843A-31 Sequence 31, Appl
33 264 11.8 3119 4 US-09-088-337B-31 Sequence 1, Appl
34 250.4 11.2 1586 1 US-08-461-244-1 Sequence 1, Appl
35 176 7.9 1050 4 US-08-681-192-1 Sequence 1, Appl
36 175.6 7.9 1200 5 PCT-US95-03032-1 Sequence 1, Appl
37 172.8 7.7 1664 4 US-09-045-583-4 Sequence 4, Appl
38 172.8 7.7 1664 4 US-09-534-185-4 Sequence 4, Appl
39 171.8 7.7 1137 4 US-09-045-583-6 Sequence 6, Appl
40 171.8 7.7 1137 4 US-09-534-185-6 Sequence 6, Appl
41 167.6 7.5 1200 5 PCT-US92-02977-1 Sequence 1, Appl
42 160 7.2 2577 4 US-09-266-464-1 Sequence 1, Appl
43 155.2 7.0 2085 3 US-09-299-843A-65 Sequence 65, Appl
44 155.2 7.0 2085 4 US-09-088-337B-65 Sequence 65, Appl
45 151.4 6.8 1106 5 PCT-US92-02977-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-450-393A-1
; Sequence 1, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..1161
; US-08-450-393A-1

Query Match 100.0%; Score 2232; DB 1; Length 2232;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGATTGAACAAAGGACGATTTCCCGACATATCCCAACATGCTGTCCACATCTGTTCT 60
Db 1 GGATTGAACAAAGGACGATTTCCCGACATATCCCAACATGCTGTCCACATCTGTTCT 60
QY 61 CGGTTTATCAGAAATACCAAGGAGCGGTGAAGAAGTCAACACCTTTTGGATTATGAT 120
Db 61 CGGTTTATCAGAAATACCAAGGAGCGGTGAAGAAGTCAACACCTTTTGGATTATGAT 120
QY 121 TAGGGTCTCCCTGCTATATAATTTGAGTGAAGCAAAATTTGGGGCCCAACTCTGCTCGG 180
Db 121 TAGGGTCTCCCTGCTATATAATTTGAGTGAAGCAAAATTTGGGGCCCAACTCTGCTCGG 180
QY 181 CTCTACTCGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCTCATCTTA 240
Db 181 CTCTACTCGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCTCATCTTA 240
QY 241 ATAACTGCAAAAAGCTGGAAGTCTGACATGCAATTTACCTGCTCAACCTGGCCATCTCT 300
Db 241 ATAACTGCAAAAAGCTGGAAGTCTGACATGCAATTTACCTGCTCAACCTGGCCATCTCT 300
QY 301 GATCTGTTTTTCTTACTCTCCCATTTGGGCTCACCTGCTGCAAAATGAGTGGGTC 360
Db 301 GATCTGTTTTTCTTACTCTCCCATTTGGGCTCACCTGCTGCAAAATGAGTGGGTC 360
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Db 361 TTTGGGAATGCAATGTCAAATATTACAGAGGCTGTATCACATCGGTTATTTGGCGGA 420
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Db 421 ATCTCTTTCATCATCTCTGCAAAATGATAGATACCTGGCTATTGTCATGCTGTTT 480
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Db 481 GCTTTTAAAGCAGGAGGCTGACCTTTGGGTTGGTGACAAAGTGTATCACTGGTGGTG 540
QY 541 GCTGTGTTTGGCTCTGTCAGGAATCATCTTTTACATAATGTCAGAAAGATTCGTGT 600
Db 541 GCTGTGTTTGGCTCTGTCAGGAATCATCTTTTACATAATGTCAGAAAGATTCGTGT 600
QY 601 TATGCTGTGGGCTTTATTTTCCAGGATGGAATATTTCCACACAATATGAGGAAC 660
Db 601 TATGCTGTGGGCTTTATTTTCCAGGATGGAATATTTCCACACAATATGAGGAAC 660
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Db 661 ATTTTGGGCTGCTGCTGCTGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 ACCCTGCTTCCGCTGTCGAAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
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QY 781 ATCATGATTTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
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Db 841 TTCCAGGAATTTCTCGGCTGAGTAACTGTAAGACCACTGCACTGCACTGCACTGCACTG 900
QY 901 CAGGTGACAGAGTCTTTGGGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 1141 CTTTCAGGACAAAAGAGGAGCTAGAGACAGAAATGACAGATCTCTGCTTTGGAATACACA 1200
QY 1201 CGTCTGGCTTTCAGATGCTGATTCACAGTGTGAATCTTGGTGTCTACGTTTACAGGCA 1260
Db 1201 CGTCTGGCTTTCAGATGCTGATTCACAGTGTGAATCTTGGTGTCTACGTTTACAGGCA 1260
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Db 1261 GGAAGGCTGAGAGGAGAGACTCCAGCTGGGTTGGAAAACAGATATTTTCCAAACTACCT 1320
QY 1321 TCCAGTCTCTCATTTTGAATACAGGCATAGAGTTCAGACTTTTAAATAGTAAAAAT 1380
Db 1321 TCCAGTCTCTCATTTTGAATACAGGCATAGAGTTCAGACTTTTAAATAGTAAAAAT 1380
QY 1381 AAAATTAAGCTGAAAACCTGAACTGTAATGTGTAAGAGTATAGTTGAGTTGCTAT 1440
Db 1381 AAAATTAAGCTGAAAACCTGAACTGTAATGTGTAAGAGTATAGTTGAGTTGCTAT 1440
QY 1441 CATGTCAAACGTAAGTGTCTGTTAGTACAGAGATATTTAGTCTTACGCTTTGAGCTTAAGA 1500
Db 1441 CATGTCAAACGTAAGTGTCTGTTAGTACAGAGATATTTAGTCTTACGCTTTGAGCTTAAGA 1500
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Db 1561 AGGAGTGTGAAGTGTGATGCTGTTGGGAGACTGCTGAGTCAACCAATAGTTGATTTGGC 1620
QY 1621 ATGATGCTGTTGAATACAGTATACGCTTCCATCGCTGCTCATCTGATGCTGATGCTGATG 1680
Db 1621 ATGATGCTGTTGAATACAGTATACGCTTCCATCGCTGCTCATCTGATGCTGATGCTGATG 1680
QY 1681 CTCTCAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 CTCTCAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
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Db 1741 GTTTTAAATCAGATTCGAGTGTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 CTAAATTTCCAGTGGGAACTCTTAATCAAAATTTGGCTTCTAATCAAAAGCTTTTAAACCCCT 1860
Db 1801 CTAAATTTCCAGTGGGAACTCTTAATCAAAATTTGGCTTCTAATCAAAAGCTTTTAAACCCCT 1860
QY 1861 ATTGGTAAAGAAATGGAAGTGGAGAGCTCCCTGAGTAAAGTAAAGAAAGCTTTTAAACCCCT 1920
Db 1861 ATTGGTAAAGAAATGGAAGTGGAGAGCTCCCTGAGTAAAGTAAAGAAAGCTTTTAAACCCCT 1920
QY 1921 CGAGCCAAAGTAAAGATTTCTTATGTTGGCCAGTGTCTTCTGATCTGATGCTGATGCTGATG 1980
Db 1921 CGAGCCAAAGTAAAGATTTCTTATGTTGGCCAGTGTCTTCTGATCTGATGCTGATGCTGATG 1980
QY 1981 AAACACTGGGCTTCTAGAACCCAGGCAACTTTGGGAACTAGACTCCCAAGCTGGACTATGSC 2040
Db 1981 AAACACTGGGCTTCTAGAACCCAGGCAACTTTGGGAACTAGACTCCCAAGCTGGACTATGSC 2040
QY 2041 TCTACTTTTCAGGCGACATGCTTAAAGAGTTCAGAAAGAGTTCAGAAAGAGTTCAGAAAGAG 2100
Db 2041 TCTACTTTTCAGGCGACATGCTTAAAGAGTTCAGAAAGAGTTCAGAAAGAGTTCAGAAAGAG 2100
QY 2101 TTTTACCTTCATATATTTGATGATCTTAATGATGATGATGATGATGATGATGATGATGATGAT 2160
Db 2101 TTTTACCTTCATATATTTGATGATCTTAATGATGATGATGATGATGATGATGATGATGATGAT 2160
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2161 TCAAAATGTAATACTGTTTAAACAACATGATTGGAAAAATAAATCAATGCTATAACTA 2220

2161 TCAAAATGTAATACTGTTTAAACAACATGATTGGAAAAATAAATCAATGCTATAACTA 2220

QY 2221 TGTGATAAAG 2232
|||||

RESULT 2

```

US-08-446-669-1
; Sequence 1, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAAMULIN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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Query Match	100.0%;	Score 2232;	DB 3;	Length 2232;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2232: Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	

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QY		
1	GGATTGAACAGGAGCGCATTTCCCGATGACATCCACACATGCTGTCCACATCTCGTTCT	60
Db		
61	CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACCTTTTGGATTATATGAT	120
QY		
61	CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACCTTTTGGATTATATGAT	120
Db		
121	TACGGTGCCTCCCTGTGATAAAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCCG	180
QY		
121	TACGGTGCCTCCCTGTGATAAAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCCG	180
Db		

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;
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..1161
; PCT-US95-00476-1

Query Match 100.0%; Score 2232; DB 5; Length 2232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAGGACGATTTCCCGAGTACATCCACACATGCTGCTCCACATCTGTTCT 60
DB 1 GGATTGAACAGGACGATTTCCCGAGTACATCCACACATGCTGCTCCACATCTGTTCT 60
QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACCTTTTGTATTATGAT 120
DB 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACCTTTTGTATTATGAT 120
QY 121 TACGGTGTCTCCCTGTCATAAATTTGAGTGAAGCAAAATGGGGCCCAACTCCTGCTCGG 180
DB 121 TACGGTGTCTCCCTGTCATAAATTTGAGTGAAGCAAAATGGGGCCCAACTCCTGCTCGG 180
QY 181 CTCTACTCGTGGTGTTCATCTTTGTTGGTGGCAACATGCTGGTGGTCTCATCTTA 240
DB 181 CTCTACTCGTGGTGTTCATCTTTGTTGGTGGCAACATGCTGGTGGTCTCATCTTA 240
QY 241 ATAACTGCAGAAAGCTGAAGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300
DB 241 ATAACTGCAGAAAGCTGAAGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300
QY 301 GATCTGCTTTTCTTATTCTCTCCATCTGGGCTCACCTGCTGCAATGAGTGGGTC 360
DB 301 GATCTGCTTTTCTTATTCTCTCCATCTGGGCTCACCTGCTGCAATGAGTGGGTC 360
QY 361 TTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGA 420
DB 361 TTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCACATCGGTTATTTTGGCGGA 420
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RESULT 3

PCT-US95-00476-1

; Sequence 1, Application PC/TUS9500476

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

Matches	980:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
QY	1	GGATTGAACACAGGAGCGCATTTCCCGACGTACATCACAAACATGCTGTGCACATCTCGTTCT	60					
Db	42	GGATTGAACAGGAGCGCATTTCCCGAGTACATCACAAACATGCTGTGCACATCTCGTTCT	100					
QY	61	CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACACTTTTTTGATTATGAT	120					
Db	102	CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACACTTTTTTGATTATGAT	160					
QY	121	TACGGTGCTCCCTGTGCATAAATTTGACGTGAAGCAAAATGGGGGCCAACCTCGTCGCCCTCG	180					
Db	162	TACGGTGCTCCCTGTGCATAAATTTGACGTGAAGCAAAATGGGGGCCAACCTCGTCGCCCTCG	220					
QY	181	CTCTACTGCGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGTGTCGTCCTCATCTTA	240					
Db	222	CTCTACTGCGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGTGTCGTCCTCATCTTA	280					
QY	241	ATAAAGTCGAAAAGCTCGAAGTGTCTCACTGACATTAATTACCTGTCTCAACCTGGCCATCTCT	3000					
Db	282	ATAAAGTCGAAAAGCTCGAAGTGTCTCACTGACATTAATTACCTGTCTCAACCTGGCCATCTCT	3410					
QY	301	GATCGCTTTTCTTATTTACTCTCCCATTTGGGCTCACCTCTGTCGAAATGAGTGGGTC	3600					
Db	342	GATCGCTTTTCTTATTTACTCTCCCATTTGGGCTCACCTCTGTCGAAATGAGTGGGTC	4010					
QY	361	TTTGGGAATGCAATGTGCAAAATTTATCACAGGCGTGTATCACATCGGTTATTTTGGCGGA	4200					
Db	402	TTTGGGAATGCAATGTGCAAAATTTATCACAGGCGTGTATCACATCGGTTATTTTGGCGGA	4610					
QY	421	ATCTTCTTCATCATCTCCTCGACAAATCGATAGATACCTGGCTATTCTCCATGCTGTGTTT	4800					
Db	462	ATCTTCTTCATCATCTCCTCGACAAATCGATAGATACCTGGCTATTCTCCATGCTGTGTTT	5210					
QY	481	GCCTTTAAAGCCAGAGCGGTACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTGGTG	5400					
Db	522	GCCTTTAAAGCCAGAGCGGTACCTTTGGGGTGGTGACAAGTGTGATCACCTGGTGGTG	5810					
QY	541	GCTGTGTTTGTCTCTGCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCGTGTT	6000					
Db	582	GCTGTGTTTGTCTCTGCCAGGAATCATCTTTACTAAATGCCAGAAAGAAATTCGTGTT	6410					
QY	601	TATGTCGTGGCCCTTATTTTCCAGGAGATGGAATATTTTCCACACATAATGAGGAAC	6600					

US-08-446-669-3

Query Match 43.9%; Score 980; DB 3; Length 1979;
Best Local Similarity 100.0%; Pred. No. 2.3e-270;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 60
DB 42 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 101
QY 61 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 120
DB 102 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 161
QY 121 TACGGTGTCCCTGTGCATATAATTTGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 180
DB 162 TACGGTGTCCCTGTGCATATAATTTGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 221
QY 181 CTCTACTCGCTGTGTTCATCTTTGTTGGGCAACATGCTGTGTCTCATCTCTA 240
DB 222 CTCTACTCGCTGTGTTCATCTTTGTTGGGCAACATGCTGTGTCTCATCTCTA 281
QY 241 ATAAACTGCAAAAGCTGAAGTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 300
DB 282 ATAAACTGCAAAAGCTGAAGTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 341
QY 301 GATCTGCTTTTCTTATTACTCTCCATCTGCTGCTCAAAATGAGTGGGTC 360
DB 342 GATCTGCTTTTCTTATTACTCTCCATCTGCTGCTCAAAATGAGTGGGTC 401
QY 361 TTTGGGAATGCAATGCAAAATTTACAGAGGCTGTATCACATCGSTTATTTTGGCGGA 420
DB 402 TTTGGGAATGCAATGCAAAATTTACAGAGGCTGTATCACATCGSTTATTTTGGCGGA 461
QY 421 ATCTTCTTCATATCTCTGCAATCGATAGATACCTGTGCTATTTGCCATGCTGTCTT 480
DB 462 ATCTTCTTCATATCTCTGCAATCGATAGATACCTGTGCTATTTGCCATGCTGTCTT 521
QY 481 GCTTTTAAAGCCAGGAGGTCACCTTTTGGGCTGTGACAGTGTGATCACCCTGGTGGTG 540
DB 522 GCTTTTAAAGCCAGGAGGTCACCTTTTGGGCTGTGACAGTGTGATCACCCTGGTGGTG 581
QY 541 GCTGTGTCTTCTGTGCCAGGAATCATCTTTTACTAAATGCCAGAAAGATTTCTGTT 600
DB 582 GCTGTGTCTTCTGTGCCAGGAATCATCTTTTACTAAATGCCAGAAAGATTTCTGTT 641
QY 601 TATGCTGTGGCCCTTATTTTCCACAGGATGGAATTAATTTCCACAAATTAAGAGAAC 660
DB 642 TATGCTGTGGCCCTTATTTTCCACAGGATGGAATTAATTTCCACAAATTAAGAGAAC 701
QY 661 ATTTTGGGCTGTGCTGCCGCTGCTCATGCTGCTACTGCTACTCGGGAATCCTGAAA 720
DB 702 ATTTTGGGCTGTGCTGCCGCTGCTCATGCTGCTACTGCTACTCGGGAATCCTGAAA 761
QY 721 ACCCTGCTCGGTGTGCAAAAGGAGAGGATAGGGCAGTGAGAGTCACTTCCACC 780
DB 762 ACCCTGCTCGGTGTGCAAAAGGAGAGGATAGGGCAGTGAGAGTCACTTCCACC 821
QY 781 ATCATGATGTTTACTTCTTCTGGAATCCCTTATACATTTGATCTCTCTGACACC 840
DB 822 ATCATGATGTTTACTTCTTCTGGAATCCCTTATACATTTGATCTCTCTGACACC 881
QY 841 TTCAGGAATTTTCGGCTGAGTAACTGTGAAGAGCAGCTCACTGACCAAGCCACG 900
DB 882 TTCAGGAATTTTCGGCTGAGTAACTGTGAAGAGCAGCTCACTGACCAAGCCACG 941
QY 901 CAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCTCAATCCCATCATCTATGCCCTC 960
DB 942 CAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCTCAATCCCATCATCTATGCCCTC 1001
QY 961 GTTGGGGAAGTTCAGAG 980
DB 1002 GTTGGGGAAGTTCAGAG 1021

RESULT 6
PCT-US95-00476-3
Sequence 3, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 81..1160
PCT-US95-00476-3

Query Match 43.9%; Score 980; DB 5; Length 1979;
Best Local Similarity 100.0%; Pred. No. 2.3e-270;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 60
DB 42 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 101
QY 61 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 120
DB 102 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 161
QY 121 TACGGTGTCCCTGTGCATATAATTTGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 180
DB 162 TACGGTGTCCCTGTGCATATAATTTGAGCGGTGAAGAGTCCACACCTTTTTCATTATGAT 221
QY 181 CTCTACTCGCTGTGTTCATCTTTGTTGGGCAACATGCTGTGTCTCATCTCTA 240
DB 222 CTCTACTCGCTGTGTTCATCTTTGTTGGGCAACATGCTGTGTCTCATCTCTA 281
QY 241 ATAAACTGCAAAAGCTGAAGTGTGACTGACATTTTACTGCTCAACCTGGCCATCTCT 300
DB 282 ATAAACTGCAAAAGCTGAAGTGTGACTGACATTTTACTGCTCAACCTGGCCATCTCT 341
QY 301 GATCTGCTTTTCTTATTACTCTCCATCTGCTGCTCAAAATGAGTGGGTC 360

Db 342 GATCTGCTTTTCTTATTAATCTCCCATTTGGGCTCACTGCTGCAAAATCAGTGGGTC 401
QY 361 TTTGGGAATCAATGTGCAAAATTAATCAGAGGCTGTATCATCATCGGTATTTGGCGGA 420
Db 402 TTTGGGAATCAATGTGCAAAATTAATCAGAGGCTGTATCATCATCGGTATTTGGCGGA 461
QY 421 ATCTTCTTCATCAATCCCTGACAAATGATAGATACCTGGCTATTTGCCATGCTGTGTT 480
Db 462 ATCTTCTTCATCAATCCCTGACAAATGATAGATACCTGGCTATTTGCCATGCTGTGTT 521
QY 481 GCTTTAAAGCCAGGAGGCTCACTTTGGGCTGTGACAAAGTGTGATCACTGCTGTGTT 540
Db 522 GCTTTAAAGCCAGGAGGCTCACTTTGGGCTGTGACAAAGTGTGATCACTGCTGTGTT 581
QY 541 GCTGTGTTGCTTCTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGTT 600
Db 582 GCTGTGTTGCTTCTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGTT 641
QY 601 TATGCTGTGGCCCTTATTTTCCACGAGGATGGAATTAATTTCCACACAATAATGAGGAAC 660
Db 642 TATGCTGTGGCCCTTATTTTCCACGAGGATGGAATTAATTTCCACACAATAATGAGGAAC 701
QY 661 ATTTTGGGCTGTGCTGCGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 702 ATTTTGGGCTGTGCTGCGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
QY 721 ACCCTGCTTGGTGCGAAACGAGAGAGAGGATAGGAGGATAGGAGGATAGGAGGATAGGAGG 780
Db 762 ACCCTGCTTGGTGCGAAACGAGAGAGAGGATAGGAGGATAGGAGGATAGGAGGATAGGAGG 821
QY 781 ATCATGATTTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 822 ATCATGATTTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
QY 841 TTCCAGGAATTTCTGGGCTGAGTAACTGTGAAAGCAGGATCACTGAGGAGGATCACTGAGG 900
Db 882 TTCCAGGAATTTCTGGGCTGAGTAACTGTGAAAGCAGGATCACTGAGGAGGATCACTGAGG 941
QY 901 CAGGTGACAGACATCTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 942 CAGGTGACAGACATCTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
QY 961 GTTGGGAGAGTTCAGAG 980
Db 1002 GTTGGGAGAGTTCAGAG 1021

RESULT 7

US-09-517-605-8

; Sequence 8, Application US/09517605

; Patent No. 6391567

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeek, Tneo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO

; FILE OF INVENTION: CELLS

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/09/517,605

; CURRENT FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 1059

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-517-605-8

Query Match

Best Local Similarity 28.5%; Score 635.6; DB 4; Length 1059;

Matches 738; Conservative 0; Mismatches 134; Indels 12; Gaps 1;

QY 110 TTGATTATGATTACGGTGTCCCTGCTCATATAAATTTGAGTGAAGCAAAATTTGGGCGCCCAAC 169
Db 35 TCGATTATGATTACGGGCGCCCTGCAAAAAATCAATGTTGAAGCAAAATCGCAGCGCCGC 94
QY 170 TCTGCTCGCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 229
Db 95 TCTGCTCGCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 154
QY 230 TCTCATCTTAATAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAA 289
Db 155 TCTGCTGCTGATTAATGCAAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAA 214
QY 290 TGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349
Db 215 TGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
QY 350 ATGAGTGGGCTTTGGGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 409
Db 275 CCCAGTGGGCTTTGGGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 334
QY 410 ATTTTGGGGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 469
Db 335 TCTTCTCTGGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 394
QY 470 ATGCTGCTGCTTAAAGCCAGGAGGCTGACCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
Db 395 ATGCTGCTGCTTAAAGCCAGGAGGCTGACCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
QY 530 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
Db 455 CTTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 590 AAGATTCTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 637
Db 515 AAGTTCTTCAATATGAGGAACTTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
QY 638 ATTTTCCACAAATTAATGAGGAACTTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 697
Db 575 ATTTTCCAGACATTAAGATAGTCACTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
QY 698 TCTGCTACTGGGAATCTGAAACCCCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 757
Db 635 TCTGCTACTGGGAATCTTAAAACTCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
QY 758 GGGCAGTGAGAGTCACTTCCACCATCATGATTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 817
Db 695 GGGCTGAGGCTTATCTTCCATCATGATTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 754
QY 818 ACATTGCTATCTCTGAAACACCTTCCAGGAATTTCTTGGGCTGCTGCTGCTGCTGCTGCTGCT 877
Db 755 ACATTGCTATCTCTGAAACACCTTCCAGGAATTTCTTGGGCTGCTGCTGCTGCTGCTGCTGCT 814
QY 878 CCAGTCAACTGGACCAACCCAGGAGTGCAGAGACTTTGGGATGCTGCTGCTGCTGCTGCTGCT 937
Db 815 CTAACAGGTTGGACCAACCCAGGAGTGCAGAGACTTTGGGATGCTGCTGCTGCTGCTGCTGCT 874
QY 938 TCAATCCCATCATCTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
Db 875 TCAACCCCATCATCTATGCTTCTTGGGAGAGGTTTCAGAGC 918

RESULT 8

US-08-724-984A-3

; Sequence 3, Application US/08724984A

; Patent No. 6388055

; GENERAL INFORMATION:

; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon

; TITLE OF INVENTION: No. 6388055el Mouse Genomic clone of the CC-

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

Query Match	28.3%;	Score	632.6;	DB	3;	Length	1376;
Best Local Similarity	83.4%;	Pred. No.	4.5e-171;				
Matches	735;	Conservative	0;	Mismatches	134;	Indels	12;
Gaps	1;						
QY	113	ATTATGATTACGGTGCCTCCCTGTATAAATTTGACGTGCAAGCAAAATTTGGGGCCCAACTCC	172				
DB	277	ATTATTTATACATCGAGCCCTGCCAAAAATCAATGTGAAGCAAAATCGACCCCGCCTCC	336				
QY	173	TGCCTCGCCTTACTTCGCTGGTGTTCATCTTTTGGTTTGTGGGCAACATGCTGTGCTGCC	232				
DB	337	TGCCTCGCCTTACTTCACTACCTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGTGTCATCC	396				
QY	233	TCATCTTAATAAACTGCAGAAAAGCTGGAAGTGCTTTGACTGACATTTACTGCTCAACCTGG	292				
DB	397	TCATCCTGATAAACTGCAGAAAAGCTGAAGAGCATGACTGACATCTACTGCTCAACCTGG	456				
QY	293	CCATCTCTGATCTGCTTTTCTTATTAATCTCCCAATTTGTGGGCTCACTCTGCTGCAAAATG	352				
DB	457	CCATCTCTGACCTGTGTTTTTCTTCTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCC	516				
QY	353	AGTGGGTCTTTGGGAATGCAATGTGCAAAATTTATTCACAGGGCTGTATCACATCGGTTATT	412				
DB	517	AGTGGGACTTTGGAAATACAAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT	576				
QY	413	TTGGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATACATACCTTGGCTATTGTCCATG	472				
DB	577	TCCTTGGAAATCTTCTTCATCATCTCTCTGACAAATCGATAGTAGTACCTTGGCTGTGCTCCATG	636				
QY	473	CTGTGTTTGCCTTTAAAAAGCCAGGACGGTCAACCTTTGGGGTGTGTGACAAGTGTGATCACCT	532				
DB	637	CTGTGTTTGCCTTTAAAAGCCAGGACGGTCAACCTTTGGGGTGTGTGACAAGTGTGATCACTT	696				
QY	533	GGTTGGTGGCTGTGTTTGTCTTCTGTGCCAGGAATCACTTTACTAAATGCCAGAAAAG	592				
DB	697	GGGTGGTGGCTGTGTTTGGCTCTCTCCAGGAATCACTTTACCAAGATCTCAAAAAG	756				

42	Db	1355GGAAATCTTCTTCATCATCTCTGACAAATGATAGATACCTGGCTGTATGTGCCATG	471
43	Db	TCCTCGGAATCTTCTTCATCATCTCTGACAAATCGATAGTAGTACCTGGCTGTGCTGCCATG	472
44	Qy	CTGTGTTTGGCTTTTAAAGCCAGGACGGTCACCTTTGGGTGGTGACAAAGTGATGACACCT	473
45	Db	CTGTGTTTGGCTTTTAAAGCCAGGACGGTCACCTTTGGGTGGTGACAAAGTGATGATCATTT	474
46	Qy	GGTTGGTGGCTGTGTTGCTTCTGTGCCAGGAATCATCTTTACTTAATGCCAGAAAGAAG	475
47	Db	GGGTGGTGGCTGTGTTGGCTCTCCAGGAATCATCTTTACAGATCTCAAAAAGAAG	476

QY 593 ATTCTGTTTANGTCTGTGGCCCTTATTTTCCA-----CGAGGATGGAATAATT 640
Db 757 GTCTTCATTACACCTGCAGCTCTCAATTTCCATACACAGTACAGTATCAATTTCTGGAAGAATT 816
QY 641 TCCACACAATAAGGAGACATTTTGGGGCTGTGCTCGCGCTGCTCATCATGTCATCT 700
Db 817 TCAGACATTAAGATAGTCAATCTTGGGGCTGTGCTCGCGCTGCTCATGTCATCT 876
QY 701 GCTACACGGGAATCCCTGAACACCTGCTTCGGGTGCTCGAAGAGAGAGAGCATAGGG 760
Db 877 GCTACTCGGGAATCCCTGAACACCTGCTTCGGGTGCTCGAAGAGAGAGAGCATAGGG 936
QY 761 CAGTGAGAGTCACTTCCACCATCATGATGTTTACCTTCTCTGAGTCCCTTATAACA 820
Db 937 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTCTCTCTGAGGCTCCCTTACAACA 996
QY 821 TTGTCATCTCCCTGAACACCTTCCAGGAATCTTCCGGCTGAGTAACTGTGAAGACACCA 880
Db 997 TTGTCCTTCTCCCTGAACACCTTCCAGGAATCTTCCGGCTGAGTAACTGTGAAGACACCA 1056
QY 881 GTCAACTGTACCAAGCCAGCTGACAGAGTCTTGGGATGACTCTTGGGATGACTCTGCTGCATCA 940
Db 1057 ACAGTTGGACCAAGCTATGAGGTGACAGAGTCTTGGGATGAGTCACTGCTGCATCA 1116
QY 941 ATCCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 981
Db 1117 ACCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 1157

RESULT 11

US-08-833-752-2

; Sequence 2, Application US/08833752

; Patent No. 6448375

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; APPLICANT: PARMENTIER, MARC

; APPLICANT: VASSART, GILBERT

; APPLICANT: LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/833.752

; FILING DATE: 9-APR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1477 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 240..1295

; US-08-833-752-2

Query Match 28.3%; Score 632.6; DB 4; Length 1477;
Best Local Similarity 83.4%; Pred. No. 4.7e-171;
Matches 735; Conservative 0; Mismatches 134; Indels 12; Gaps 1;

QY 113 ATTATGATTACGGTCTCCCTGTCATATAAATTTGACGTGAAGCAAAATTTGGGGCCCACTCC 172
Db 277 ATTATTTATACATCGGAGCCCTGCGCAAAATCAATGTGAAGCAAAATCGCAGCGCCCTCC 336
QY 173 TGCCTCCGCTCTACTCCCTGCTGTCATCTTTGCTTTTGTGGGCAACATGCTGTCGTC 232
Db 337 TGCCTCCGCTCTACTCCCTGCTGTCATCTTTGCTTTTGTGGGCAACATGCTGTCATCC 396
QY 233 TCATCTTAATAAAGCTGCAAAAGCTGAAGTCTTGTGACTGACATTTACCTGCTCAACCTGG 292
Db 397 TCATCTGATTAAGCTGCAAAAGCTGAAGTCTTGTGACTGACATTTACCTGCTCAACCTGG 456
QY 293 CCATCTCTGATCTCTTTTCTTATTAATCTCTCCCATTTGTGGGCTCACTCTGCTGCAATG 352
Db 457 CCATCTCTGATCTCTTTTCTTATTAATCTCTCCCATTTGTGGGCTCACTCTGCTGCAATG 516
QY 353 AGTGGGCTTTTGGGAATGCAATGTCRAATTTATTCACAGGCTGTATCACATCGGTTATT 412
Db 517 AGTGGGCTTTTGGGAATGCAATGTCRAATTTATTCACAGGCTGTATTCATGAGCTTCT 576
QY 413 TTGGCGGAATCTTCTTCATCATCTCTGACAAATCGATAGATACCTGCTATTTGTCATG 472
Db 577 TCTCTGGAATCTTCTTCATCATCTCTGACAAATCGATAGATACCTGCTATTTGTCATG 636
QY 473 CTGTGTTTGTCTTAAAGCCAGGAGGTCACCTTTTGGGGTGGTGACAAAGTGTGATCACT 532
Db 637 CTGTGTTTGTCTTAAAGCCAGGAGGTCACCTTTTGGGGTGGTGACAAAGTGTGATCACT 696
QY 533 GGTGGTGGCTGTGTTTCTCTGTCGCCAGGAATCATCTTTACTAAATGCCAAGAAAGAG 592
Db 697 GGTGGTGGCTGTGTTTCTCTGTCGCCAGGAATCATCTTTACTAAATGCCAAGAAAGAG 756
QY 593 ATTCTGTTTATGCTGTGGCCCTTATTTTCCA-----CGAGGATGGAATAATT 640
Db 757 GTCITTCATTACACCTGTCAGCTCTCATTTTCCATACAGTACAGTATCAATTTCTGGAAGAATT 816
QY 641 TCCACACAATAATGAGGACATTTTGGGGCTGTGCTCGCGCTGCTCATCATGTCATCT 700
Db 817 TCCAGACATTAAGATAGTCAATCTTGGGGCTGTGCTCGCGCTGCTCATGTCATCT 876
QY 701 GCTACTCGGAATCCTGAAACCCCTGCTTCGGTGTGCGAAGAGAGAGAGAGCATAGGG 760
Db 877 GCTACTCGGAATCCTGAAACCCCTGCTTCGGTGTGCGAAGAGAGAGAGAGCATAGGG 936
QY 761 CAGTGAGAGTCACTTTCACCATCATGATGTTTACTTCTCTCTGAGTCCCTTATAACA 820
Db 937 CTGTGAGGCTTATCTTTCACCATCATGATGTTTACTTCTCTCTGAGTCCCTTATAACA 996
QY 821 TTGTCATCTCTGTCGACACCTTCCAGGAATTTCTCGGCTGAGTAACTGTGAAGACACCA 880
Db 997 TTGTCCTTCTCTGTCGACACCTTCCAGGAATTTCTTGGGCTGATATTAATTCAGTAGTCT 1056
QY 881 GTCAACTGGACCAAGCCAGCTGAGTGTGACAGACTCTTGGGATGACTCTTGGGATGACTCT 940
Db 1057 ACAGTTGGACCAAGCTATGAGGTGACAGAGTCTTGGGATGAGTCACTGCTGCATCA 1116
QY 941 ATCCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 981
Db 1117 ACCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 1157

RESULT 12

US-08-861-105-13

; Sequence 13, Application US/08861105

; Patent No. 6258527

; GENERAL INFORMATION:

; APPLICANT: LITTMAN, DAN R.

; APPLICANT: DENG, HONGKUI

APPLICANT: ELLMEIER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCE ADDRESSES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3383 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-13

Query Match 28.3%; Score 632.6; DB 4; Length 3383;
Best Local Similarity 83.4%; Pred. No. 7.3e-171;
Matches 735; Conservative 0; Mismatches 134; Indels 12; Gaps 1;
QY 113 ATTATGATGAGGCTGCTCCCTGTCTATAAATTGACGTGAAGCAAAATGGGGCCCACTCC 172
DB 92 ATTATATACATCGAGCCCTGCCAAAATAATGTAAGCAAAATCGAGCCCGCTCC 151
QY 173 TGCCTCGCTACTCGCTGCTGTTCATCTTTGTTGTTGGGCAACATGCTGGTCTCC 232
DB 152 TGCCTCGCTACTCGCTGCTGTTCATCTTTGTTGTTGGGCAACATGCTGGTCTCC 211
QY 233 TCATCTTAATAAATGCAAAAGCTGAAGTCTGACGTGACATTTACCTGCTCAACCTGG 292
DB 212 TCATCTGATTAATGCAAAAGGCTGAAGACATGACATGACATCTACCTGCTCAACCTGG 271
QY 293 CCATCTCTGATCTGCTTTTCTTATTACTCTCCCATCTGGGCTCAGCTCTGCAATG 352
DB 272 CCATCTCTGACCTGTTTCTCTTCTACTGTCCTCTGCGCTCAGCTGCTGCGGCC 331
QY 353 AGTGGGCTTTGGAAATGCAATGCAAAATTAATTCACAGGCTGTATCAGATCGGTTAT 412
DB 332 AGTGGGCTTTGGAAATACAAATGTGTCAACTCTTGACAGGCTCTATTTATAGCTCT 391

QY 413 TTGGCGGAATCTTCTTCATCATCTCCTCTGACAATCGATAGATACCTGGCTATTTCATG 472
DB 392 TCTGTAATCTTCTTCATCATCTCCTCTGACAATCGATAGATACCTGGCTATTTCATG 451
QY 473 CTGTGTTTCTTAAAGCCAGGCTGACCTTTGGGGTGGTGACAAGTGTGTATCCT 532
DB 452 CTGTGTTTCTTAAAGCCAGGCTGACCTTTGGGGTGGTGACAAGTGTGTATCCT 511
QY 533 GGTGTTGCTGTGTTTGTCTTGTCTCCAGGAATCATCTTAAATGCAAGAAAG 592
DB 512 GGTGTTGCTGTGTTTGTCTTGTCTCCAGGAATCATCTTAAATGCAAGAAAG 571
QY 593 ATTCTGTTTATGCTGTGCTGCTTATTTTCCA-----CGAGGATGGAATTAAT 640
DB 572 GTCTTCATTAACACCTGACGCTCTCATTTTCCATACAGTACAGTATCAATTTGGAAGAAT 631
QY 641 TCCACACAATAATGAGGAACATTTTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
DB 632 TCCACACAATAATGAGGAATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
QY 701 GCTACTCGGAATCTGAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
DB 692 GCTACTCGGAATCTGAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 751
QY 761 CAGTGAGAGTATCTTCCACCATCATGATGTTTACTTTCTTCTGCTGCTGCTGCTGCTGCT 820
DB 752 CTGTGAGGCTTATCTTCCACCATCATGATGTTTACTTTCTTCTGCTGCTGCTGCTGCT 811
QY 821 TTGTCTTCTCTGAAACACCTTCCAGGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
DB 812 TTGTCTTCTCTGAAACACCTTCCAGGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
QY 881 GTCACTGAGCAACGACGAGTGTGACAGACTTGTGGGACTGCTGCTGCTGCTGCTGCTGCT 940
DB 872 ACAGGTTGGACCAAGCTATGAGGTGACAGACTTGTGGGACTGCTGCTGCTGCTGCTGCT 931
QY 941 ATCCCATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
DB 932 ACCCATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972

RESULT 13
US-08-575-967A-1
Sequence 1, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662

Db 872 ACAGTTGGACCAAGCTATGACAGTATGACAGAGACTTTGGGATGACGACCTGCTGCATCA 931

QY 941 ATCCCATCATCTATGCTTCTGTTGGGAGAAAGTTTCAGAAC 981

Db 932 ACCCATCATCTATGCTTCTGTTGGGAGAAAGTTTCAGAAC 972

RESULT 14

US-09-293-170-3

; Sequence 3, Application US/09293170

; Patent No. 6383777

; GENERAL INFORMATION:

; APPLICANT: Breyer, Richard M.

; APPLICANT: Ma, Lijun

; APPLICANT: Kennedy, Chris

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD

; FILE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS

; FILE REFERENCE: 22000.0094

; CURRENT APPLICATION NUMBER: US/09/293,170

; CURRENT FILING DATE: 1999-04-16

; EARLIER APPLICATION NUMBER: 60/081,989

; EARLIER FILING DATE: 1998-04-16

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 5674

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (300)...(1616)

; OTHER INFORMATION: Description of Artificial Sequence:/note -

; OTHER INFORMATION: synthetic construct

US-09-293-170-3

Query Match 28.3%; Score 632.6; DB 4; Length 5674;

Best Local Similarity 83.4%; Pred. No. 9.7e-171;

Matches 735; Conservative 0; Mismatches 134; Indels 12; Gaps 1;

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

Db 631 TGCTCGGCTCTACTCTGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 690

QY 233 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 292

Db 691 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 750

QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

Db 751 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 810

QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

Db 811 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATTCATGCTGCTCT 870

QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

Db 631 TGCTCGGCTCTACTCTGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 690

QY 233 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 292

Db 691 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 750

QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

Db 751 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 810

QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

Db 811 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATTCATGCTGCTCT 870

QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

Db 631 TGCTCGGCTCTACTCTGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 690

QY 233 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 292

Db 691 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 750

QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

Db 751 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 810

QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

Db 811 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATTCATGCTGCTCT 870

QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

Db 631 TGCTCGGCTCTACTCTGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 690

QY 233 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 292

Db 691 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 750

QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

Db 751 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 810

QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

Db 811 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATTCATGCTGCTCT 870

QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

Db 631 TGCTCGGCTCTACTCTGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 690

QY 233 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 292

Db 691 TCATCTTAATAAAGCTCAAAAGCTGAAGTGTGCTGACTGACATTTACCTGCTCAACCTGG 750

QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

Db 751 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 810

QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

Db 811 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATTCATGCTGCTCT 870

QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

QY 113 ATTATGATTACGGTCTCCCTGTCAATAAATTTGACGTGAAGCAAAATTTGGGCGCAACTCC 172

Db 571 ATTATATACATCGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGCAGCCGCTCC 630

QY 173 TGCTCGGCTCTACTCGCTGGTTCATCTTTGGTTTGGGCAACATGCTGCTGCTCC 232

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QY 353 AGTGGGCTTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTATCACATCGGTATT 412

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QY 413 TTGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 472

Db 871 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTGCTGCTGCT 930

QY 473 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

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Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

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QY 293 CCATCTCTGATCTGCTTTTCTTATTAATCTCTCCCATTTGGGCTCACTGCTGCAATG 352

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Db 931 CTGCTGTTGCTTTAAAGCCAGGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCT 990

QY 533 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592

Db 991 GGTGGGCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

QY 593 ATTCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640

